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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/276,268

DATE: 03/31/1999
TIME: 14:03:13

Input Set: I276268.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

1 <110> APPLICANT: Strachan, Lorna
2 Sleeman, Matthew
3 Abernethy, Nevin
4 Onrust, Rene
5 Kumble, Anand
6 Murison, Greg
7 <120> TITLE OF INVENTION: Compounds isolated from stromal cells
8 and methods for their use
9 <130> FILE REFERENCE: 11000.1037
10 <140> CURRENT APPLICATION NUMBER: US/09/276,268
11 <141> CURRENT FILING DATE: 1999-03-25
12 <160> NUMBER OF SEQ ID NOS: 20
13 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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15 <211> LENGTH: 803
16 <212> TYPE: DNA
17 <213> ORGANISM: Mouse
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21 ctgcgggctg tggatctgtc gggaaactcc ctgaccagct tccaaaagtt caagggcagt 180
22 ttggcccttc ggactctcga cctccgcaga aactctctca cggccctccc tcagagggtt 240
23 gtgtccgagc agcctctgag gggctctgag accatctacc tcagccagaa cccttatgac 300
24 tgctgtgggg tggaaggatg gggggccctg cagcagcact tcaagactgt tgcggacttg 360
25 tccatggtca cttgcaacct ctcttccaag atcgtccgtg tgggtggagct gcccgaggc 420
26 ctgcctcagg gctgtaagt ggaacagggtg gacactggtc tcttctacct cgtgtctatc 480
27 ctgcccagct gcctcacct gctgggtggc tgtactgtcg tcttctctac ttttaagaag 540
28 cctttgcttc aggtcatcaa gagccgctgc cactggctct ccatatactg acccgtgtgc 600
29 caaggctaga gacttggttt ttctctgagg atgcgtctct ccgctggatc tttacttttg 660
30 caggggtcga gtgtgatgca ttgaagggtt aaactgaaat ttgaaagagt tccatcctca 720
31 gtcccattaa cttctcctcc catccgtgtg atttatectc attgtcctgg tgaaatattt 780
32 attaaacgac attctgtgag att 803
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34 <211> LENGTH: 689
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36 <213> ORGANISM: Mouse
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39 <222> LOCATION: (35)...(556)
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42 Met Ala Pro Ala Asn Leu Gly
43 1 5
44 ctg acg ccg cac tgg gtg atg ctc ctc ggt gcc gtg ctg ctg ttg ctt 103

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45      Leu Thr Pro His Trp Val Met Leu Leu Gly Ala Val Leu Leu Leu Leu
46              10              15              20
47      ctg tcc gga gcc tcc gcg cag gaa cct ccg aga gtg ggt tgc tct gag      151
48      Leu Ser Gly Ala Ser Ala Gln Glu Pro Pro Arg Val Gly Cys Ser Glu
49              25              30              35
50      tac aca aac aga tcc tgt gaa gag tgc ctc agg aat gtc tcc tgt ctg      199
51      Tyr Thr Asn Arg Ser Cys Glu Glu Cys Leu Arg Asn Val Ser Cys Leu
52              40              45              50              55
53      tgg tgc aat gag aac aag gcg tgt atg gac tac cca gtg agg aaa atc      247
54      Trp Cys Asn Glu Asn Lys Ala Cys Met Asp Tyr Pro Val Arg Lys Ile
55              60              65              70
56      ttg ccc cct gct tct ctc tgt aaa ttg agt tcc gct cgc tgg ggc gta      295
57      Leu Pro Pro Ala Ser Leu Cys Lys Leu Ser Ser Ala Arg Trp Gly Val
58              75              80              85
59      tgc tgg gtg aac ttc gag gcc ttg atc atc acc atg tgc gtc ctg ggg      343
60      Cys Trp Val Asn Phe Glu Ala Leu Ile Ile Thr Met Ser Val Leu Gly
61              90              95              100
62      ggc tct gtg ctc ctg ggc atc act gtg tgc tgc tgc tac tgc tgc cgc      391
63      Gly Ser Val Leu Leu Gly Ile Thr Val Cys Cys Cys Tyr Cys Cys Arg
64              105              110              115
65      cgg aag aag agc cgg aag cca gac aag agc gat gag cgg gcc atg aga      439
66      Arg Lys Lys Ser Arg Lys Pro Asp Lys Ser Asp Glu Arg Ala Met Arg
67      120              125              130              135
68      gag cag gag gag agg aga gtg cgg cag gag gaa agg agg gcg gaa atg      487
69      Glu Gln Glu Glu Arg Arg Val Arg Gln Glu Glu Arg Arg Ala Glu Met
70              140              145              150
71      aag tca aga cat gat gaa atc agg aaa aaa tac ggt ctg ttt aaa gaa      535
72      Lys Ser Arg His Asp Glu Ile Arg Lys Lys Tyr Gly Leu Phe Lys Glu
73              155              160              165
74      caa aac ccg tat gag aag ttc taagggtggct ggcacacact tgtgggtggat      586
75      Gln Asn Pro Tyr Glu Lys Phe
76              170
77      cgtgcagttc cagagtttcc tgggaatgca ctccccagca gagcctgcag agacctcacc      646
78      accatggcca cccttgacct ggggtgatccc tcagcctcta ctg      689
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82      <213> ORGANISM: Mouse
83      <400> SEQUENCE: 3
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86      cccatcaaca tgggtcctgt gcccgctccc tatgtccccc ctctgcccac cgtgcgtgtc      180
87      aactatgact ttggccacat gcacgtgccc ctggagcaca acctgcccac gcactttggc      240
88      ccccaaccac ggcacgcctt ctgacaccca aagccctgtc agccgtgccc agtctgtagg      300
89      agggcccagt ctcatcttct gtaggggggt gaaggcctcc attccctctc gaaagtggac      360
90      gcgtgtcttc ctgctcttac ctttgcaagg tccatgctcc ttcagggtctg atgccctctg      420
91      ggtgctgatt gtcactgggc caattatagg gcagctccct agtctgccat cttagcagcc      480
92      aatccagtgg ccctgaccat gaagcaaggc ctctaactgt ttgccatact tctccccag      540
93      cagcccaatg aaagcccagg gggaaatggc ctaccatccc taagccaggg ctctctcctt      600
94      gttgcccaag gcccaactta      619

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98 <213> ORGANISM: Mouse
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101 <222> LOCATION: (46)...(849)
102 <221> NAME/KEY: sig_peptide
103 <222> LOCATION: (46)...(150)
104 <400> SEQUENCE: 4
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106                                     Met Ala Leu Gly
107                                     -35
108   ttt tct caa cgc tcc cgt atg gtg gcc gcg ggt gcc ggg gtg acc cgg      105
109   Phe Ser Gln Arg Ser Arg Met Val Ala Ala Gly Ala Gly Val Thr Arg
110   -30                               -25                               -20
111   ctg cta gtg ctc ttg ctg atg gta gcc gcg gct cct agc aga gcc cga      153
112   Leu Leu Val Leu Leu Leu Met Val Ala Ala Ala Pro Ser Arg Ala Arg
113   -15                               -10                               -5                               1
114   ggc agc ggc tgc cgg gtc ggg gcc tcc gcg cgt ggg acc ggg gcc gat      201
115   Gly Ser Gly Cys Arg Val Gly Ala Ser Ala Arg Gly Thr Gly Ala Asp
116   5                               10                               15
117   ggc cgt gaa gct gag ggc tgt ggc acc gtg gct ttg ctg ctg gag cat      249
118   Gly Arg Glu Ala Glu Gly Cys Gly Thr Val Ala Leu Leu Leu Glu His
119   20                               25                               30
120   tca ttt gag ctc ggt gat gga gcc aac ttc cag aag cga ggc ttg ctg      297
121   Ser Phe Glu Leu Gly Asp Gly Ala Asn Phe Gln Lys Arg Gly Leu Leu
122   35                               40                               45
123   ctc tgg aac cag cag gat ggc acc ctg tcg gca aca cag cga cag ctc      345
124   Leu Trp Asn Gln Gln Asp Gly Thr Leu Ser Ala Thr Gln Arg Gln Leu
125   50                               55                               60                               65
126   agt gag gag gag cgt ggc cga ctc cgg gat gtg gct gct gtc aat ggc      393
127   Ser Glu Glu Glu Arg Gly Arg Leu Arg Asp Val Ala Ala Val Asn Gly
128   70                               75                               80
129   ctc tac agg gtc cgg gtc ccg agg cgg cct ggg aca ctt gat ggt tca      441
130   Leu Tyr Arg Val Arg Val Pro Arg Arg Pro Gly Thr Leu Asp Gly Ser
131   85                               90                               95
132   gaa gct ggc ggc cat gtg tct tcc ttc gtc cca gcg tgc tcc ctg gtg      489
133   Glu Ala Gly Gly His Val Ser Ser Phe Val Pro Ala Cys Ser Leu Val
134   100                              105                              110
135   gag tcg cac ctt tcg gac cag ctg acc ttg cac gtg gat gtg gct ggc      537
136   Glu Ser His Leu Ser Asp Gln Leu Thr Leu His Val Asp Val Ala Gly
137   115                              120                              125
138   aac gtg gtg ggc ctg tct gtg gtg gtg tac cct ggg ggc tgc cgg ggc      585
139   Asn Val Val Gly Leu Ser Val Val Val Tyr Pro Gly Gly Cys Arg Gly
140   130                              135                              140                              145
141   tcc gag gtg gaa gat gag gac ctg gag ctg ttc aat aca tct gtg cag      633
142   Ser Glu Val Glu Asp Glu Asp Leu Glu Leu Phe Asn Thr Ser Val Gln
143   150                              155                              160
144   ctg cgg cct ccc agc act gct cca ggc ccc gag act gca gcc ttc att      681

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145      Leu Arg Pro Pro Ser Thr Ala Pro Gly Pro Glu Thr Ala Ala Phe Ile
146                      165                      170                      175
147      gag cgc ctg gag atg gag cag gcc cag aag gcc aag aac cca cag gag      729
148      Glu Arg Leu Glu Met Glu Gln Ala Gln Lys Ala Lys Asn Pro Gln Glu
149                      180                      185                      190
150      cag aag tct ttc ttt gcc aaa tac tgg atg tac atc att cca gtt gtg      777
151      Gln Lys Ser Phe Phe Ala Lys Tyr Trp Met Tyr Ile Ile Pro Val Val
152                      195                      200                      205
153      ctg ttc ctc atg atg tgc gga gcg ccg gac gct ggg ggc cag ggc ggc      825
154      Leu Phe Leu Met Met Ser Gly Ala Pro Asp Ala Gly Gly Gln Gly Gly
155      210                      215                      220                      225
156      ggt ggg ggc ggg ggc agc agc cgg tgagcagctg tgccacctag agcccccccc      879
157      Gly Gly Gly Gly Gly Ser Ser Arg
158                      230
159      agagccagcc caagaaggag ttcttgaccc cacatttccc tattgcatga atatggaagg      939
160      ctgtcccttc agtgagccct ctggccttcc tgtaagcccc tctttctgtc cctgagcctc      999
161      tctctcatcc tgttgactga gagcttgggt ggacctccct gtagccagct cactgcaact      1059
162      gtgtccacc atgtggcact gtgtcctct gtctgctaaa caccaccag cctgccccac      1119
163      cccacccac catacacttt gggaacttgc caagctctct ccagcctctg tgcctttgcc      1179
164      ctgcaggccc cgtgcgcccc tctactgtcac tctccagccc tttgccaagg atctgtggcc      1239
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166      gtcttctttg cccccctctc tgggtcccca gaataccatg gtgacctacc actatccttt      1359
167      ctgcctttgg atgtcatagc ctggatctgt caccaggaga ggattgtggg cctccacgtt      1419
168      agtctgtgaa tgcacacttc gagtgacttg tgtgcagggt ttgagagccg gttttgcaact      1479
169      agctgctcga cagctgctgg catggccgtg ctcttgacac tgcgcgcgtg tgggcatggg      1539
170      gattgctgtg cagcctcagc tgtgttgtgt ggctgctgat taaactgtcc cctaaacagc      1599
171      aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a      1630
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173      <211> LENGTH: 1197
174      <212> TYPE: DNA
175      <213> ORGANISM: Mouse
176      <220> FEATURE:
177      <221> NAME/KEY: CDS
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179      <221> NAME/KEY: sig_peptide
180      <222> LOCATION: (346)...(420)
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183      gtgtggggcg ctcagtgata ggcgtagtga cagtgcagct gacagctaga gggatgatag      120
184      acccccaaac tagtggaact tgaagttttc ttcccagccg gttccagcct cctggaacaa      180
185      ccatgtcgcc agttttgcgc gtgccaaatt cacggcgctg cccaagcgga gctgctatct      240
186      gaattctcct tggatgtggc aaagggaaat gaacgcaaaa ggtgccgctg gaagtgtccg      300
187      acctagagaa atatgtagac cggagccctg ttaccttctt ccagc atg gac ttc ctg      357
188                                     Met Asp Phe Leu
189                                     -25
190      gtt ctc ttc ttg ttc tac ttg gcc ttc tta ttg att tgt gtt gtc ctg      405
191      Val Leu Phe Leu Phe Tyr Leu Ala Phe Leu Leu Ile Cys Val Val Leu
192      -20                      -15                      -10
193      atc tgc atc ttc aca aaa agc cag cgt ttg aag gcc gtg gtc ctt gga      453
194      Ile Cys Ile Phe Thr Lys Ser Gln Arg Leu Lys Ala Val Val Leu Gly

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Please Note:
 Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
 Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
 <223> fields of each sequence which presents at least one n or Xaa.

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195	-5	1	5	10	
196	gga gca cag gta gca ctg gtc ctt ggg tac tgc ccg gat gtg aat act				501
197	Gly Ala Gln Val Ala Leu Val Leu Gly Tyr Cys Pro Asp Val Asn Thr				
198	15	20	25		
199	gtg tta ggt gct agt ctg gaa ggc tca caa gac aag ggg atg				543
200	Val Leu Gly Ala Ser Leu Glu Gly Ser Gln Asp Lys Gly Met				
201	30	35	40		
202	tgagtcttgt ctttaatcct ggcacttggg aggctgaggc ttcggggcca gttggggcta				603
203	catcgcaaga gcctgtgtcc aaacaaacaa aacgttgtct ttttgctttg agataggtcg				663
204	aataggtcga attttcaagg ttggcttttt aaacagtgtg taatgtctgt atttggttgt				723
205	gactcctgtt tgcctagaca tgcttgtagc aggtgtgaac tcaggaggac acaagtgacc				783
206	agaaagctga gcatctagct gtcaatcttc ctttcacatt gtcccatctg tcttcccttg				843
207	ggggtcaaag caaagtgggg gcaagtagcc acgaaggggt tgacttggga ggaccctggg				903
208	gatctggagg ccaatcttga gcatggagca gacctgaggg ttagggaagc ccacgtccac				963
209	agcagcctct gcacaccccc tttccccaca gactccaaca gacacattct gtgcagtcaa				1023
210	ggtagaaatg gaggtgttct ctacacctcc taaatcctag cacttaggaa gctgaggcag				1083
211	gattatgaat tccaggctag ctcggttat gtaatgagac tgtttcaaac acagagcgga				1143
212	gccgaggaga tggctgggca gtcacagagc tgccgtgcaa ccagaactgg aggg				1197
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220	<221> NAME/KEY: sig_peptide				
221	<222> LOCATION: (2)...(46)				
222	<400> SEQUENCE: 6				
223	c atg ggc gcc gtc tgg tca gcc ctg ctg gtc ggc ggg ggt cta gct gga				49
224	Met Gly Ala Val Trp Ser Ala Leu Leu Val Gly Gly Gly Leu Ala Gly				
225	-15	-10	-5	1	
226	gcg ctc atc ctg tgg ctg ctg cgg gga gac tct ggg gcc ccg ggg aaa				97
227	Ala Leu Ile Leu Trp Leu Leu Arg Gly Asp Ser Gly Ala Pro Gly Lys				
228	5	10	15		
229	gac ggg gtt gcg gag ccg ccg cag aag ggc gca cct cct ggg gag gct				145
230	Asp Gly Val Ala Glu Pro Pro Gln Lys Gly Ala Pro Pro Gly Glu Ala				
231	20	25	30		
232	gcg gcc ccg gga gac ggt ccg ggt ggt ggt ggc agt ggc ggc ctg agc				193
233	Ala Ala Pro Gly Asp Gly Pro Gly Gly Gly Gly Ser Gly Gly Leu Ser				
234	35	40	45		
235	cct gaa cct tcc gat cgg gag ctg gtc tcc aaa gca gag cat ctt cga				241
236	Pro Glu Pro Ser Asp Arg Glu Leu Val Ser Lys Ala Glu His Leu Arg				
237	50	55	60	65	
238	gaa agc aac gga cat ttg att tct gag agc aaa gat ctt ggt aac ctg				289
239	Glu Ser Asn Gly His Leu Ile Ser Glu Ser Lys Asp Leu Gly Asn Leu				
240	70	75	80		
241	ccg gaa gca cag cgg ctg cag aat gtt gga gca gac tgg gtc aat gcc				337
242	Pro Glu Ala Gln Arg Leu Gln Asn Val Gly Ala Asp Trp Val Asn Ala				
243	85	90	95		
244	aga gag ttt gtt cct gtt ggg aag att cca gac aca cac tcc agg gcc				385

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VERIFICATION SUMMARY
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Line	? Error/Warning	Original Text
288	W Invalid/Missing Amino Acid Numbering	
291	W "N" or "Xaa" used: Feature required	cctgcagata atgcttcctg taanctggca cttgtccc